

SEQUENCE LISTING

(1) GENERAL INFORMATION

- 5 (i) APPLICANT: University of Utrecht, Technology Foundation
- (ii) TITLE OF THE INVENTION: Vaccine
- (iii) NUMBER OF SEQUENCES: 10
- 10 (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: SmithKline Beecham, Corporate IP Department
- (B) STREET: Two, New Horizons Court,
- (C) CITY: Brentford
- 15 (D) STATE: Middlesex
- (E) COUNTRY: United Kingdom
- (F) ZIP: TW8 9EP
- (v) COMPUTER READABLE FORM:
- 20 (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0
- 25 (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- 30 (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- 35 (A) NAME: DALTON, Marcus Jonathan William
- (B) REGISTRATION NUMBER: XXXXXX
- (C) REFERENCE/DOCKET NUMBER: B45106
- (ix) TELECOMMUNICATION INFORMATION:
- 40 (A) TELEPHONE: (0181) 975 6348
- (B) TELEFAX: (0181) 975 6177

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2277 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(B) STRAIN: *Neisseria meningitidis* strain BNCV

(ix) FEATURE:

15 (A) NAME/KEY: Coding Sequence

(B) LOCATION: 100...2274

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20 TCCTGATTTT TGTTAATTCA CTATAAAAAC GGGTTGATAT TATCTGTACA TATTAATATA 60
 ATGATAATTA TTATTAATCA AATAGGAGGA AAAGTAGGG ATG TGT AAA CCG AAT 114
 Met Cys Lys Pro Asn
 1 5

25 TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTG GCA TCT TGT ATC GGC 162
 Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Ala Ser Cys Ile Gly
 10 15 20

30 GGC AAT TTC GGC GTG CAG CCT GTT GTC GAA TCA ACG CCG ACC GCG TAC 210
 Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser Thr Pro Thr Ala Tyr
 25 30 35

35 CCC GTC ACT TTC AAG TCT AAG GAC GTT CCC ACT CCG CCC CCT GCC AAA 258
 Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr Pro Pro Pro Ala Lys
 40 45 50

40 CCT TCT ATA GAA ATC ACG CCG GTC AAC CGG CCC GCC GTC GGT GCG GCA 306
 Pro Ser Ile Glu Ile Thr Pro Val Asn Arg Pro Ala Val Gly Ala Ala
 55 60 65

	ATG CGG CTG CCA AGG CGG AAT ACT GCT TTT CAT CGT GAA GAT GGC ACG	354
	Met Arg Leu Pro Arg Arg Asn Thr Ala Phe His Arg Glu Asp Gly Thr	
	70 75 80 85	
5	GAA ATT CCA AAT AGC AAA CAA GCA GAA GAA AAG CTG TCG TTT CAA GAA	402
	Glu Ile Pro Asn Ser Lys Gln Ala Glu Glu Lys Leu Ser Phe Gln Glu	
	90 95 100	
10	GGT GAT GTT CTG TTT TTA TAC GGT TCA AAA GGA AAT AAA CTT CAA CAA	450
	Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Gly Asn Lys Leu Gln Gln	
	105 110 115	
15	CTT AAA AGC GAA ATT CAT AAA CGT GAT TCC GAT GTA GAA ATT AGG ACA	498
	Leu Lys Ser Glu Ile His Lys Arg Asp Ser Asp Val Glu Ile Arg Thr	
	120 125 130	
20	TCA GAA AAG GAA AAT AAA AAA TAT GAT TAT AAA TTT GTA GAT GCA GGT	546
	Ser Glu Lys Glu Asn Lys Lys Tyr Asp Tyr Lys Phe Val Asp Ala Gly	
	135 140 145	
25	TAT GTA TAT GTA AAG GGA AAA GAT GAA ATT AAG TGG ACT TCA GAT TAC	594
	Tyr Val Tyr Val Lys Gly Lys Asp Glu Ile Lys Trp Thr Ser Asp Tyr	
	150 155 160 165	
30	AAG CAG TTT TCC AAC CGC TTA GGT TAT GAC GGT TTT GTA TAT TAT TCC	642
	Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp Gly Phe Val Tyr Tyr Ser	
	170 175 180	
35	GGA GAA CGT CCT TCC CAA TCT TTA CCG AGT GCG GGA ACG GTG GAA TAT	690
	Gly Glu Arg Pro Ser Gln Ser Leu Pro Ser Ala Gly Thr Val Glu Tyr	
	185 190 195	
40	TCT GGT AAC TGG CAA TAT ATG ACC GAT GCC AAA CGT CAT CGA GCA GGT	738
	Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala Lys Arg His Arg Ala Gly	
	200 205 210	
45	AAG GCG GTT GGC ATT GAC AAT TTG GGT TAT TAC ACA TTT TAT GGT AAC	786
	Lys Ala Val Gly Ile Asp Asn Leu Gly Tyr Tyr Thr Phe Tyr Gly Asn	
	215 220 225	
50	GAT GTT GGT GCA ACT TCT TAT GCG GCT AAG GAT GTC GAC GAA AGG GAA	834
	Asp Val Gly Ala Thr Ser Tyr Ala Ala Lys Asp Val Asp Glu Arg Glu	
	230 235 240 245	

	AAA CAT CCT GCT AAA TAT ACG GTA GAT TTC GGT AAC AAA ACC CTG ACG	882
	Lys His Pro Ala Lys Tyr Thr Val Asp Phe Gly Asn Lys Thr Leu Thr	
	250 255 260	
5	GGC GAG CTG ATT AAA AAC CAA TAT GTC AAA CCC AGT GAG AAG CAA AAA	930
	Gly Glu Leu Ile Lys Asn Gln Tyr Val Lys Pro Ser Glu Lys Gln Lys	
	265 270 275	
10	CCG CTG ACC ATT TAC AAC ATC ACT GCC GAT TTA AAC GGC AAC CGC TTT	978
	Pro Leu Thr Ile Tyr Asn Ile Thr Ala Asp Leu Asn Gly Asn Arg Phe	
	280 285 290	
	ACC GGC AGT GCC AAG GTC AAT CCT GAT TTA GCG AAA AGC CAT GCC AAT	1026
15	Thr Gly Ser Ala Lys Val Asn Pro Asp Leu Ala Lys Ser His Ala Asn	
	295 300 305	
	AAG GAG CAT TTG TTT TTC CAT GCC GAT GCC GAT CAG CGG CTT GAG GGC	1074
	Lys Glu His Leu Phe Phe His Ala Asp Ala Asp Gln Arg Leu Glu Gly	
20	310 315 320 325	
	GGT TTT TTC GGC GAT AAG GGG GAA GAG CTT GCC GGA CGG TTT ATC AGC	1122
	Gly Phe Phe Gly Asp Lys Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser	
	330 335 340	
25	AAC GAC AAC AGC GTA TTC GGT GTA TTC GCA GGC AAA CAA AAT AGC CCC	1170
	Asn Asp Asn Ser Val Phe Gly Val Phe Ala Gly Lys Gln Asn Ser Pro	
	345 350 355	
30	GTG CCG TCT GGA AAA CAC ACC AAA ATC TTG GAT TCT CTG AAA ATT TCC	1218
	Val Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys Ile Ser	
	360 365 370	
	GTT GAT GAG GCA AGT GGT GAA AAT CCC CGA CCG TTT GCC ATT TCT CCT	1266
35	Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro Phe Ala Ile Ser Pro	
	375 380 385	
	ATG CCC GAT TTT GGT CAT CCC GAC AAA CTT CTT GTC GAA GGG CAT GAA	1314
	Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly His Glu	
40	390 395 400 405	

	ATT CCT TTG GTT AGC CAA GAG AAA ACC ATC GAG CTT GCC GAC GGC AGG	1362
	Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala Asp Gly Arg	
	410 415 420	
5	AAA ATG ACC GTC AGT GCT TGT TGC GAC TTT TTG ACC TAT GTG AAA CTC	1410
	Lys Met Thr Val Ser Ala Cys Cys Asp Phe Leu Thr Tyr Val Lys Leu	
	425 430 435	
10	GGA CGG ATA AAA ACC GAA CGC CCC GCC GCC AAA CCG AAG GCG CAG GAC	1458
	Gly Arg Ile Lys Thr Glu Arg Pro Ala Ala Lys Pro Lys Ala Gln Asp	
	440 445 450	
15	GAA GAG GAT TCG GAC ATT GAT AAT GGC GAA GAA AGC GAA GAC GAA ATC	1506
	Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu Ser Glu Asp Glu Ile	
	455 460 465	
20	GGC GAT GAA GAA GAA GGC ACC GAA GAT GCA GCC GCA GGA GAT GAA GGC	1554
	Gly Asp Glu Glu Glu Gly Thr Glu Asp Ala Ala Ala Gly Asp Glu Gly	
	470 475 480 485	
25	AGC GAA GAA GAC GAA GCC ACA GAA AAC GAA GAC GGC GAA GAA GAC GAA	1602
	Ser Glu Glu Asp Glu Ala Thr Glu Asn Glu Asp Gly Glu Glu Asp Glu	
	490 495 500	
30	GCT GAA GAA CCT GAA GAA GAA TCG TCG GCA GAA GGC AAC GGC AGT TCA	1650
	Ala Glu Glu Pro Glu Glu Glu Ser Ser Ala Glu Gly Asn Gly Ser Ser	
	505 510 515	
35	AAC GCC ATC CTG CCT GTC CCG GAA GCC TCT AAA GGC AGG GAT ATC GAC	1698
	Asn Ala Ile Leu Pro Val Pro Glu Ala Ser Lys Gly Arg Asp Ile Asp	
	520 525 530	
40	CTT TTC CTG AAA GGT ATC CGC ACG GCA GAA ACG AAT ATT CCG CAA ACT	1746
	Leu Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr Asn Ile Pro Gln Thr	
	535 540 545	
45	GGA GAA GCA CGC TAT ACC GGC ACT TGG GAA GCG CGT ATC GGC AAA CCC	1794
	Gly Glu Ala Arg Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Lys Pro	
	550 555 560 565	
50	ATT CAA TGG GAC AAT CAT GCG GAT AAA GAA GCG GCA AAA GCA GTA TTT	1842
	Ile Gln Trp Asp Asn His Ala Asp Lys Glu Ala Ala Lys Ala Val Phe	
	570 575 580	

	ACC GTT GAT TTC GGC AAG AAA TCG ATT TCC GGA ACG CTG ACG GAG AAA	1890
	Thr Val Asp Phe Gly Lys Lys Ser Ile Ser Gly Thr Leu Thr Glu Lys	
	585 590 595	
5	AAC GGT GTA GAA CCT GCT TTC CGT ATT GAA AAC GGC GTG ATT GAG GGC	1938
	Asn Gly Val Glu Pro Ala Phe Arg Ile Glu Asn Gly Val Ile Glu Gly	
	600 605 610	
10	AAC GGT TTC CAT GCG ACA GCG CGC ACT CGG GAT GAC GGC ATC GAC CTT	1986
	Asn Gly Phe His Ala Thr Ala Arg Thr Arg Asp Asp Gly Ile Asp Leu	
	615 620 625	
15	TCC GGG CAG GGT TCG ACC AAA CCG CAG ATC TTC AAA GCT AAT GAT CTT	2034
	Ser Gly Gln Gly Ser Thr Lys Pro Gln Ile Phe Lys Ala Asn Asp Leu	
	630 635 640 645	
20	CGT GTA GAA GGA GGA TTT TAC GGC CCG AAG GCG GAG GAA TTG GGC GGT	2082
	Arg Val Glu Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly	
	650 655 660	
25	ATT ATT TTC AAT AAT GAT GGG AAA TCT CTT GGT ATA ACT GAA GGT ACT	2130
	Ile Ile Phe Asn Asn Asp Gly Lys Ser Leu Gly Ile Thr Glu Gly Thr	
	665 670 675	
30	GAA AAT AAA GTT GAA GCT GAT GTT GAT GTT GAT GTT GAT GTT GAT GTT	2178
	Glu Asn Lys Val Glu Ala Asp Val Asp Val Asp Val Asp Val Asp Val	
	680 685 690	
35	GAT GCT GAT GCT GAT GTT GAA CAG TTA AAA CCT GAA GTT AAA CCC CAA	2226
	Asp Ala Asp Ala Asp Val Glu Gln Leu Lys Pro Glu Val Lys Pro Gln	
	695 700 705	
35	TTC GGC GTG GTA TTC GGT GCG AAG AAA GAT AAT AAA GAG GTG GAA AAA T	2275
	Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn Lys Glu Val Glu Lys	
	710 715 720 725	
	GA	2277

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 725 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(B) STRAIN: Neisseria meningitidis strain BNCV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15

Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
1 5 10 15
Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
20 25 30
Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
35 40 45
Pro Pro Pro Ala Lys Pro Ser Ile Glu Ile Thr Pro Val Asn Arg Pro
50 55 60
Ala Val Gly Ala Ala Met Arg Leu Pro Arg Arg Asn Thr Ala Phe His
25 65 70 75 80
Arg Glu Asp Gly Thr Glu Ile Pro Asn Ser Lys Gln Ala Glu Glu Lys
85 90 95
Leu Ser Phe Gln Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Gly
100 105 110
30 Asn Lys Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asp Ser Asp
115 120 125
Val Glu Ile Arg Thr Ser Glu Lys Glu Asn Lys Lys Tyr Asp Tyr Lys
130 135 140
Phe Val Asp Ala Gly Tyr Val Tyr Val Lys Gly Lys Asp Glu Ile Lys
35 145 150 155 160
Trp Thr Ser Asp Tyr Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp Gly
165 170 175

Phe Val Tyr Tyr Ser Gly Glu Arg Pro Ser Gln Ser Leu Pro Ser Ala
 180 185 190
 Gly Thr Val Glu Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala Lys
 195 200 205
 5 Arg His Arg Ala Gly Lys Ala Val Gly Ile Asp Asn Leu Gly Tyr Tyr
 210 215 220
 Thr Phe Tyr Gly Asn Asp Val Gly Ala Thr Ser Tyr Ala Ala Lys Asp
 225 230 235 240
 Val Asp Glu Arg Glu Lys His Pro Ala Lys Tyr Thr Val Asp Phe Gly
 10 245 250 255
 Asn Lys Thr Leu Thr Gly Glu Leu Ile Lys Asn Gln Tyr Val Lys Pro
 260 265 270
 Ser Glu Lys Gln Lys Pro Leu Thr Ile Tyr Asn Ile Thr Ala Asp Leu
 275 280 285
 15 Asn Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn Pro Asp Leu Ala
 290 295 300
 Lys Ser His Ala Asn Lys Glu His Leu Phe Phe His Ala Asp Ala Asp
 305 310 315 320
 Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys Gly Glu Glu Leu Ala
 20 325 330 335
 Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val Phe Ala Gly
 340 345 350
 Lys Gln Asn Ser Pro Val Pro Ser Gly Lys His Thr Lys Ile Leu Asp
 355 360 365
 25 Ser Leu Lys Ile Ser Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro
 370 375 380
 Phe Ala Ile Ser Pro Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu
 385 390 395 400
 Val Glu Gly His Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu
 30 405 410 415
 Leu Ala Asp Gly Arg Lys Met Thr Val Ser Ala Cys Cys Asp Phe Leu
 420 425 430
 Thr Tyr Val Lys Leu Gly Arg Ile Lys Thr Glu Arg Pro Ala Ala Lys
 435 440 445
 35 Pro Lys Ala Gln Asp Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu
 450 455 460

Ser Glu Asp Glu Ile Gly Asp Glu Glu Glu Gly Thr Glu Asp Ala Ala
 465 470 475 480
 Ala Gly Asp Glu Gly Ser Glu Glu Asp Glu Ala Thr Glu Asn Glu Asp
 485 490 495
 5 Gly Glu Glu Asp Glu Ala Glu Glu Pro Glu Glu Glu Ser Ser Ala Glu
 500 505 510
 Gly Asn Gly Ser Ser Asn Ala Ile Leu Pro Val Pro Glu Ala Ser Lys
 515 520 525
 Gly Arg Asp Ile Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr
 10 530 535 540
 Asn Ile Pro Gln Thr Gly Glu Ala Arg Tyr Thr Gly Thr Trp Glu Ala
 545 550 555 560
 Arg Ile Gly Lys Pro Ile Gln Trp Asp Asn His Ala Asp Lys Glu Ala
 565 570 575
 15 Ala Lys Ala Val Phe Thr Val Asp Phe Gly Lys Lys Ser Ile Ser Gly
 580 585 590
 Thr Leu Thr Glu Lys Asn Gly Val Glu Pro Ala Phe Arg Ile Glu Asn
 595 600 605
 Gly Val Ile Glu Gly Asn Gly Phe His Ala Thr Ala Arg Thr Arg Asp
 20 610 615 620
 Asp Gly Ile Asp Leu Ser Gly Gln Gly Ser Thr Lys Pro Gln Ile Phe
 625 630 635 640
 Lys Ala Asn Asp Leu Arg Val Glu Gly Gly Phe Tyr Gly Pro Lys Ala
 645 650 655
 25 Glu Glu Leu Gly Gly Ile Ile Phe Asn Asn Asp Gly Lys Ser Leu Gly
 660 665 670
 Ile Thr Glu Gly Thr Glu Asn Lys Val Glu Ala Asp Val Asp Val Asp
 675 680 685
 Val Asp Val Asp Val Asp Ala Asp Ala Asp Val Glu Gln Leu Lys Pro
 30 690 695 700
 Glu Val Lys Pro Gln Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn
 705 710 715 720
 Lys Glu Val Glu Lys
 725

10

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (B) STRAIN: *Neisseria meningitidis* strain M981

(ix) **FEATURE:**

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...2166
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

20	ATG TGT AAA CCG AAT TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTG	48
	Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu	
	1 5 10 15	
25	GCA TCT TGC ATC GGC GGC AAT TTC GGC GTG CAG CCT GTT GTC GAA TCA	96
	Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser	
	20 25 30	
30	ACG CCG ACC GCG TAC CCC GTC ACT TTC AAG TCT AAG GAC GTT CCC ACT	144
	Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr	
	35 40 45	
35	TCG CCC CCT GCC GGG TCT TCG GTA GAA ACC ACG CCG GTC AAC CAG CCC	192
	Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Gln Pro	
	50 55 60	
40	GCC GTC GGT GCG GCA ATG CGG CTG TTG AGA CGG AAT ACT GCT TTT CAT	240
	Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Thr Ala Phe His	
	65 70 75 80	
40	CGT GAA GAT GGC ACG GCA ATT CCC GAT AGC AAA CAA GCA GAA GAA AAG	288
	Arg Glu Asp Gly Thr Ala Ile Pro Asp Ser Lys Gln Ala Glu Glu Lys	
	85 90 95	

11

	CTG TCG TTT AAA GAA GGT GAT GTT CTG TTT TTA TAC GGT TCA AAA GAA	336
	Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Glu	
	100 105 110	
5	AAT AAA CTT CAA CAA CTT AAA AGC GAA ATT CAT AAA CGT AAT CCT GAG	384
	Asn Lys Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asn Pro Glu	
	115 120 125	
10	GCA AGC ATT ACC ACA TCG GAA AAT GAA AAT AAA AAA TAT AAT TAT CGG	432
	Ala Ser Ile Thr Thr Ser Glu Asn Glu Asn Lys Lys Tyr Asn Tyr Arg	
	130 135 140	
15	TTT GTC AGT GCC GGT TAT GTG TTT ACT AAA AAC GGA AAA GAT GAA ATT	480
	Phe Val Ser Ala Gly Tyr Val Phe Thr Lys Asn Gly Lys Asp Glu Ile	
	145 150 155 160	
20	GAG AAA ACA TCG GAT GAA AAG CAG TTT TCT AAT CGT TTA GGC TAT GAC	528
	Glu Lys Thr Ser Asp Glu Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp	
	165 170 175	
25	GGT TTT GTA TAT TAT CTC GGA GAA CAT CCT TCC CAA TCT TTA CCG AGC	576
	Gly Phe Val Tyr Tyr Leu Gly Glu His Pro Ser Gln Ser Leu Pro Ser	
	180 185 190	
30	GCG GGA ACG GTG AAA TAT TCC GGC AAC TGG CAA TAT ATG ACC GAT GCC	624
	Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala	
	195 200 205	
35	ATA CGT CAT CGG AGA GGT AAG GGG GTT TCC AGT GTG GAT TTG GGT TAT	672
	Ile Arg His Arg Arg Gly Lys Gly Val Ser Ser Val Asp Leu Gly Tyr	
	210 215 220	
40	ACC ACA TAT TAT GGT AAT GAA ATT GGG GCA GCT TCT TAT GAG GCT AGG	720
	Thr Thr Tyr Tyr Gly Asn Glu Ile Gly Ala Ala Ser Tyr Glu Ala Arg	
	225 230 235 240	
45	GAT GCC GAT GGC CGG GAA AAA CAT CCT GCC GAA TAT ACG GTT AAT TTC	768
	Asp Ala Asp Gly Arg Glu Lys His Pro Ala Glu Tyr Thr Val Asn Phe	
	245 250 255	
50	GAC AAA AAA AAC CTG GAA GGT AAG TTG ATT AAA AAT CAG TAT GTG CAA	816
	Asp Lys Lys Asn Leu Glu Gly Lys Leu Ile Lys Asn Gln Tyr Val Gln	
	260 265 270	

	AAG AGA GAT GAT CCT AAA AAT CCA CTG ACC ATT TAC AAC ATT ACC GCA	864
	Lys Arg Asp Asp Pro Lys Asn Pro Leu Thr Ile Tyr Asn Ile Thr Ala	
	275 280 285	
5	ACA TTG GAC GGC AAC CGC TTT ACC GGC AGT GCC AAA GTT AGC ACC GAG	912
	Thr Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Ser Thr Glu	
	290 295 300	
10	GTG AAG ACG CAA CAC GCT GAT AAA GAA TAT TTG TTT TTC CAT ACC GAT	960
	Val Lys Thr Gln His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr Asp	
	305 310 315 320	
15	GCC GAT CAG CGG CTT GAG GGC GGT TTT TTC GGC GAT AAC GGA GAA GAG	1008
	Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Asn Gly Glu Glu	
	325 330 335	
20	CTT GCC GGG CGG TTT ATC AGT AAC GAC AAC AGC GTA TTC GGC GTG TTC	1056
	Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val Phe	
	340 345 350	
25	GCA GGC AAA CAA AAA ACA GAG ACA GCA AAC GCA TCA GAT ACA AAT CCT	1104
	Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn Pro	
	355 360 365	
30	GCC CTG CCG TCT GGA AAA CAC ACC AAA ATC TTG GAT TCT CTA AAA ATT	1152
	Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys Ile	
	370 375 380	
35	TCC GTT GAC GAG GCG ACT GAT GAC CAT GCC CGT AAG TTT GCC ATT TCC	1200
	Ser Val Asp Glu Ala Thr Asp Asp His Ala Arg Lys Phe Ala Ile Ser	
	385 390 395 400	
40	ACT ATG CCC GAT TTT GGT CAT CCC GAC AAA CTT CTT GTC GAA GGG CGT	1248
	Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly Arg	
	405 410 415	
40	GAA ATT CCT TTG GTT AGC CAA GAG AAA ACC ATC GAG CTT GCC GAC GGC	1296
	Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala Asp Gly	
	420 425 430	

	AGG AAA ATG ACC ATC CGT GCT TGT TGC GAT TTT CTG ACC TAT GTG AAA	1344
	Arg Lys Met Thr Ile Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val Lys	
	435 440 445	
5	CTC GGA CGG ATA AAA ACC GAC CGC CCC GCC GTC AAA CCG AAG GCG CAG	1392
	Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Val Lys Pro Lys Ala Gln	
	450 455 460	
10	GAT GAA GAG GAT TCG GAC ATT GAT AAT GGC GAA GAA AGC GAA GAC GAA	1440
	Asp Glu Glu Asp Ser Asp Ile Asp Asn Gly Glu Glu Ser Glu Asp Glu	
	465 470 475 480	
15	ATT TCC GAA GAT GAT AAC GGC GAA GAT GAA GTC ACC GAA GAA GAG GAA	1488
	Ile Ser Glu Asp Asp Asn Gly Glu Asp Glu Val Thr Glu Glu Glu Glu	
	485 490 495	
20	GCT GAA GAA ACC GAA GAA GAA ACT GAT GAA GAC GAA GAG GAA GAA CCC	1536
	Ala Glu Glu Thr Glu Glu Glu Thr Asp Glu Asp Glu Glu Glu Glu Pro	
	500 505 510	
25	GAA GAA ACT GAA GAA ACT GAA GAA ACT GAA GAA ACT GAA GAA ACT GAA	1584
	Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu Glu Thr Glu	
	515 520 525	
30	GAA ACT GAA GAA AAA TCG CCG ACA GAA GAA GGC AAC GGC GGT TCA GGC	1632
	Glu Thr Glu Glu Lys Ser Pro Thr Glu Glu Gly Asn Gly Gly Ser Gly	
	530 535 540	
35	AGC ATC CTG CCC ACT CCG GAA GCC TCT AAA GGC AGG GAC ATC GAC CTT	1680
	Ser Ile Leu Pro Thr Pro Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu	
	545 550 555 560	
40	TTC CTG AAA GGT ATC CGC ACG GCG GAA GCC GAC ATT CCG CAA ATT GGA	1728
	Phe Leu Lys Gly Ile Arg Thr Ala Glu Ala Asp Ile Pro Gln Ile Gly	
	565 570 575	
45	AAA GCA CGC TAT ACC GGC ACT TGG GAA GCG CGT ATC GGC GTG CCG GAT	1776
	Lys Ala Arg Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Val Pro Asp	
	580 585 590	
50	AAG AAA GGC GAA CAG CTA GAT GGC ACT ACG TCC ATT CAA AAG GAT AGC	1824
	Lys Lys Gly Glu Gln Leu Asp Gly Thr Thr Ser Ile Gln Lys Asp Ser	
	595 600 605	

5	TAT GCG AAT CAA GCG GCA AAA GCA GAA TTT GAC GTT GAT TTT GGT GCG	1872
	Tyr Ala Asn Gln Ala Ala Lys Ala Glu Phe Asp Val Asp Phe Gly Ala	
	610 615 620	
	AAG TCG CTT TCA GGT AAG TTG ACA GAA AAA AAT GAT ACA CAC CCC GCT	1920
	Lys Ser Leu Ser Gly Lys Leu Thr Glu Lys Asn Asp Thr His Pro Ala	
10	625 630 635 640	
	TTT TAT ATT GAA AAA GGT GTG ATT GAT GGC AAC GGT TTC CAC GCT TTG	1968
	Phe Tyr Ile Glu Lys Gly Val Ile Asp Gly Asn Gly Phe His Ala Leu	
	645 650 655	
	GCG CGT ACT CGT GAA AAT GGT GTT GAT TTG TCT GGG CAA GGT TCG ACT	2016
15	Ala Arg Thr Arg Glu Asn Gly Val Asp Leu Ser Gly Gln Gly Ser Thr	
	660 665 670	
	AAT CCC CAA AGT TTT AAA GCC AGT AAT CTT CTC GTA GAA GGA GGA TTT	2064
	Asn Pro Gln Ser Phe Lys Ala Ser Asn Leu Leu Val Glu Gly Gly Phe	
	675 680 685	
20	TAT GGT CCG CAG GCG GCA GAG TTG GGT GGT AAT ATT ATC GAC AGT GAC	2112
	Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Asn Ile Ile Asp Ser Asp	
	690 695 700	
	CGG AAA ATC GGC GTG GTA TTC GGT GCG AAG AAA GAT ATG CAG GAG GTG	2160
	Arg Lys Ile Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val	
25	705 710 715 720	
	GAA AAA TGA	2169
	Glu Lys	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(B) STRAIN: Neisseria meningitidis strain M981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
 1 5 10 15
 Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
 20 25 30
 Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
 35 40 45
 Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Gln Pro
 50 55 60
 Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Thr Ala Phe His
 65 70 75 80
 Arg Glu Asp Gly Thr Ala Ile Pro Asp Ser Lys Gln Ala Glu Glu Lys
 85 90 95
 Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser Lys Glu
 100 105 110
 Asn Lys Leu Gln Gln Leu Lys Ser Glu Ile His Lys Arg Asn Pro Glu
 115 120 125
 Ala Ser Ile Thr Thr Ser Glu Asn Glu Asn Lys Lys Tyr Asn Tyr Arg
 130 135 140
 Phe Val Ser Ala Gly Tyr Val Phe Thr Lys Asn Gly Lys Asp Glu Ile
 145 150 155 160
 Glu Lys Thr Ser Asp Glu Lys Gln Phe Ser Asn Arg Leu Gly Tyr Asp
 165 170 175
 Gly Phe Val Tyr Tyr Leu Gly Glu His Pro Ser Gln Ser Leu Pro Ser
 180 185 190
 Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala
 195 200 205
 Ile Arg His Arg Arg Gly Lys Gly Val Ser Ser Val Asp Leu Gly Tyr
 210 215 220

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	Thr	Thr	Tyr	Tyr	Gly	Asn	Glu	Ile	Gly	Ala	Ala	Ser	Tyr	Glu	Ala	Arg
	225					230				235						240
	Asp	Ala	Asp	Gly	Arg	Glu	Lys	His	Pro	Ala	Glu	Tyr	Thr	Val	Asn	Phe
				245						250					255	
5	Asp	Lys	Lys	Asn	Leu	Glu	Gly	Lys	Leu	Ile	Lys	Asn	Gln	Tyr	Val	Gln
				260					265					270		
	Lys	Arg	Asp	Asp	Pro	Lys	Asn	Pro	Leu	Thr	Ile	Tyr	Asn	Ile	Thr	Ala
			275					280					285			
	Thr	Leu	Asp	Gly	Asn	Arg	Phe	Thr	Gly	Ser	Ala	Lys	Val	Ser	Thr	Glu
10		290					295					300				
	Val	Lys	Thr	Gln	His	Ala	Asp	Lys	Glu	Tyr	Leu	Phe	Phe	His	Thr	Asp
	305					310					315					320
	Ala	Asp	Gln	Arg	Leu	Glu	Gly	Gly	Phe	Phe	Gly	Asp	Asn	Gly	Glu	Glu
				325						330					335	
15	Leu	Ala	Gly	Arg	Phe	Ile	Ser	Asn	Asp	Asn	Ser	Val	Phe	Gly	Val	Phe
			340						345					350		
	Ala	Gly	Lys	Gln	Lys	Thr	Glu	Thr	Ala	Asn	Ala	Ser	Asp	Thr	Asn	Pro
		355						360					365			
	Ala	Leu	Pro	Ser	Gly	Lys	His	Thr	Lys	Ile	Leu	Asp	Ser	Leu	Lys	Ile
20		370					375					380				
	Ser	Val	Asp	Glu	Ala	Thr	Asp	Asp	His	Ala	Arg	Lys	Phe	Ala	Ile	Ser
	385					390					395					400
	Thr	Met	Pro	Asp	Phe	Gly	His	Pro	Asp	Lys	Leu	Leu	Val	Glu	Gly	Arg
				405					410					415		
25	Glu	Ile	Pro	Leu	Val	Ser	Gln	Glu	Lys	Thr	Ile	Glu	Leu	Ala	Asp	Gly
			420						425					430		
	Arg	Lys	Met	Thr	Ile	Arg	Ala	Cys	Cys	Asp	Phe	Leu	Thr	Tyr	Val	Lys
		435						440					445			
	Leu	Gly	Arg	Ile	Lys	Thr	Asp	Arg	Pro	Ala	Val	Lys	Pro	Lys	Ala	Gln
30		450					455					460				
	Asp	Glu	Glu	Asp	Ser	Asp	Ile	Asp	Asn	Gly	Glu	Glu	Ser	Glu	Asp	Glu
	465					470				475					480	
	Ile	Ser	Glu	Asp	Asp	Asn	Gly	Glu	Asp	Glu	Val	Thr	Glu	Glu	Glu	Glu
				485					490					495		
35	Ala	Glu	Glu	Thr	Glu	Glu	Glu	Thr	Asp	Glu	Asp	Glu	Glu	Glu	Glu	Pro
				500					505					510		
	Glu	Glu	Thr	Glu	Glu	Thr	Glu	Glu	Thr	Glu	Glu	Thr	Glu	Glu	Thr	Glu
		515						520					525			
	Glu	Thr	Glu	Glu	Lys	Ser	Pro	Thr	Glu	Glu	Gly	Asn	Gly	Gly	Ser	Gly
40		530					535				540					
	Ser	Ile	Leu	Pro	Thr	Pro	Glu	Ala	Ser	Lys	Gly	Arg	Asp	Ile	Asp	Leu
	545					550					555				560	

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[illegible]

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2226 base pairs

5 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (vi) ORIGINAL SOURCE:

(B) STRAIN: *Neisseria meningitidis* strain H44/76

(ix) **FEATURE:**

(A) NAME/KEY: Coding Sequence

15 (B) LOCATION: 1...2223

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

20 ATG TGT AAA CCG AAT TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTG 48
Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
1 5 10 15

25 GCA TCT TGT ATT GGC GGC AAT TTC GGC GTG CAG CCT GTT GTC GAA TCA 96
Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
20 25 30

ACG CCG ACC GCG TAC CCC GTC ACT TTC AAG TCT AAG GAC GTT CCC ACT 144
Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr

CCG CCC CCT GCC AAA CCT TCT ATA GAA ACC ACG CCG GTG CCG TCA ACC 192
Pro Pro Pro Ala Lys Pro Ser Ile Glu Thr Thr Pro Val Pro Ser Thr
50 55 60

GGG CCT GCC GTC GGT GCG GCA ATG CGG CTG TTG AGG CGG ATT TTC GCA 240
Gly Pro Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Ile Phe Ala
65 70 75 80

40 ACT TCT GAT AAG GTT GGC AAT GAT TTT CCA AAT AGC AAA CAA GCA GAA 288
 Thr Ser Asp Lys Val Gly Asn Asp Phe Pro Asn Ser Lys Gln Ala Glu
 85 90 95

	GAA AAG CTG TCG TTT AAA GAA GGT GAT GTT CTG TTT TTA TAC GGT TCA	336
	Glu Lys Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser	
	100 105 110	
5	AAA AAA GAT AAA CTT CAG TGG CTT AAG GAT AAA ATT CAT CAA CGC AAT	384
	Lys Lys Asp Lys Leu Gln Trp Leu Lys Asp Lys Ile His Gln Arg Asn	
	115 120 125	
10	CCT AAT GTA GAA ATT AGG ACA TCA GAA AAT GAA AAT AAA AAA TAT GGT	432
	Pro Asn Val Glu Ile Arg Thr Ser Glu Asn Glu Asn Lys Lys Tyr Gly	
	130 135 140	
	TAT GAA TTT GTG GAT GCC GGT TAT GTA TAT ACT AAA AAC GGA ACA GAT	480
	Tyr Glu Phe Val Asp Ala Gly Tyr Val Tyr Thr Lys Asn Gly Thr Asp	
15	145 150 155 160	
	GAA ATT GAG TGG ACT TCA AAT CGC AAG CAG TTT TCT AAT CGT TTT GGC	528
	Glu Ile Glu Trp Thr Ser Asn Arg Lys Gln Phe Ser Asn Arg Phe Gly	
	165 170 175	
20	TAC GAC GGT TTT GTA TAT TAT TCC GGA GAA CAT CCT TCC CAA TCT TTA	576
	Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu His Pro Ser Gln Ser Leu	
	180 185 190	
25	CCG AGC GCG GGA ACG GTG CAA TAT TCC GGT AAC TGG CAA TAT ATG ACC	624
	Pro Ser Ala Gly Thr Val Gln Tyr Ser Gly Asn Trp Gln Tyr Met Thr	
	195 200 205	
30	GAT GCC ATA CGT CAT CGA ACA GGA AAA GCA GGA GAT CCT AGC GAA GAT	672
	Asp Ala Ile Arg His Arg Thr Gly Lys Ala Gly Asp Pro Ser Glu Asp	
	210 215 220	
	TTG GGT TAT CTC GTT TAT TAC GGT CAA AAT GTC GGA GCA ACT TCT TAT	720
	Leu Gly Tyr Leu Val Tyr Tyr Gly Gln Asn Val Gly Ala Thr Ser Tyr	
35	225 230 235 240	
	GCT GCG ACT GCC GAC GAC CGG GAG GGA AAA CAT CCT GCC GAA TAT ACG	768
	Ala Ala Thr Ala Asp Asp Arg Glu Gly Lys His Pro Ala Glu Tyr Thr	
	245 250 255	
40	GTT GAT TTC GAT AAG AAA ACT TTG ACG GGT CAA TTA ATT AAA AAT CAG	816
	Val Asp Phe Asp Lys Lys Thr Leu Thr Gly Gln Leu Ile Lys Asn Gln	
	260 265 270	

	TAT GTG CAA AAG AAA ACC GAT GAA AAG AAA CCA CTG ACC ATT TAC GAC	864
	Tyr Val Gln Lys Lys Thr Asp Glu Lys Lys Pro Leu Thr Ile Tyr Asp	
	275 280 285	
5	ATT ACC GCA ACA TTG GAC GGC AAC CGC TTT ACC GGC AGT GCC AAA GTT	912
	Ile Thr Ala Thr Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val	
	290 295 300	
10	AAC ACC GAG TTG AAG ACG AGC CAC GCT GAT AAA GAG CAT TTG TTT TTC	960
	Asn Thr Glu Leu Lys Thr Ser His Ala Asp Lys Glu His Leu Phe Phe	
	305 310 315 320	
15	CAT ACC GAT GCC GAT CAG CGG CTT GAG GGC GGT TTT TTC GGC GAT AAG	1008
	His Thr Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys	
	325 330 335	
20	GGG GAA GAG CTT GCC GGA CGG TTT ATC AGC AAC GAC AAC AGC GTA TTC	1056
	Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe	
	340 345 350	
25	GGC GTA TTC GCA GGC AAA AAA ACA AAC GCA TCA AAC GCA GCA GAT ACA	1104
	Gly Val Phe Ala Gly Lys Lys Thr Asn Ala Ser Asn Ala Ala Asp Thr	
	355 360 365	
30	AAT CCT GCT ATG CCG TCT GAA AAA CAC ACC AAA ATC TTG GAT TCT CTG	1152
	Asn Pro Ala Met Pro Ser Glu Lys His Thr Lys Ile Leu Asp Ser Leu	
	370 375 380	
35	AAA ATT TCC GTT GAC GAG GCG ACG GAT AAA AAT GCC CGC CCG TTT GCC	1200
	Lys Ile Ser Val Asp Glu Ala Thr Asp Lys Asn Ala Arg Pro Phe Ala	
	385 390 395 400	
40	ATT TCC CCT CTG CCC GAT TTT GGC CAT CCC GAC AAA CTC CTT GTC GAA	1248
	Ile Ser Pro Leu Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu	
	405 410 415	
40	GGG CGT GAA ATT CCT TTG GTT AGC CAA GAG AAA ACC ATC GAG CTT GCC	1296
	Gly Arg Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala	
	420 425 430	

	GAC GGC AGG AAA ATG ACC GTC CGT GCT TGT TGC GAT TTT CTG ACC TAT	1344
	Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr	
	435 440 445	
5	GTG AAA CTC GGA CGG ATA AAA ACT GAC CGC CCA GCA AGT AAA CCA AAG	1392
	Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys Pro Lys	
	450 455 460	
10	GCG GAA GAT AAA GGG AAG GAT GAA GAG GAT ACA GGC GTT GGT AAC GAC	1440
	Ala Glu Asp Lys Gly Lys Asp Glu Glu Asp Thr Gly Val Gly Asn Asp	
	465 470 475 480	
15	GAA GAA GGC ACG GAA GAT GAA GCC GCA GAA GGC AGC GAA GGA GGC GAA	1488
	Glu Glu Gly Thr Glu Asp Glu Ala Ala Glu Gly Ser Glu Gly Gly Glu	
	485 490 495	
20	GAC GAA ATC GGC GAT GAA GGA GGA GGT GCG GAA GAC GAA GCC GCA GAA	1536
	Asp Glu Ile Gly Asp Glu Gly Gly Gly Ala Glu Asp Glu Ala Ala Glu	
	500 505 510	
25	AAC GAA GGC GGC GAA GAA GAC GAA GCT GAA GAA CCT GAA GAA CCC GAA	1584
	Asn Glu Gly Gly Glu Glu Asp Glu Ala Glu Glu Pro Glu Glu Pro Glu	
	515 520 525	
30	GAA GAA TCG CCG GCA GAA GGC GGC GGT GGT GGT TCA GAC GGC ATC CTG	1632
	Glu Glu Ser Pro Ala Glu Gly Gly Gly Gly Gly Ser Asp Gly Ile Leu	
	530 535 540	
35	CCC GCT CCG GAA GCT CCT AAA GGC AGG GAT ATC GAC CTT TTC CTG AAA	1680
	Pro Ala Pro Glu Ala Pro Lys Gly Arg Asp Ile Asp Leu Phe Leu Lys	
	545 550 555 560	
40	GGT ATC CGC ACG GCG GAA GCC GAC ATT CCG CAA ACT GGA AAA GCA CGC	1728
	Gly Ile Arg Thr Ala Glu Ala Asp Ile Pro Gln Thr Gly Lys Ala Arg	
	565 570 575	
45	TAT ACC GGC ACT TGG GAA GCG CGT ATC AGC AAA CCC ATT CAA TGG GAC	1776
	Tyr Thr Gly Thr Trp Glu Ala Arg Ile Ser Lys Pro Ile Gln Trp Asp	
	580 585 590	
50	AAT CAT GCG GAT AAA AAA GCG GCA AAA GCA GAA TTT GAC GTT GAT TTC	1824
	Asn His Ala Asp Lys Lys Ala Ala Lys Ala Glu Phe Asp Val Asp Phe	
	595 600 605	

	GGC GAG AAA TCG ATT TCC GGA ACG CTG ACG GAG AAA AAC GGT GTA CAA	1872
	Gly Glu Lys Ser Ile Ser Gly Thr Leu Thr Glu Lys Asn Gly Val Gln	
	610 615 620	
5	CCT GCT TTC CAT ATT GAA AAC GGC GTG ATT GAG GGC AAT GGT TTC CAC	1920
	Pro Ala Phe His Ile Glu Asn Gly Val Ile Glu Gly Asn Gly Phe His	
	625 630 635 640	
10	GCG ACA GCG CGC ACT CGG GAT AAC GGC ATC AAT CTT TCG GGA AAT GAT	1968
	Ala Thr Ala Arg Thr Arg Asp Asn Gly Ile Asn Leu Ser Gly Asn Asp	
	645 650 655	
	TCG ACT AAT CCT CCA AGT TTC AAA GCC AAT AAT CTT CTT GTA ACA GGC	2016
15	Ser Thr Asn Pro Pro Ser Phe Lys Ala Asn Asn Leu Leu Val Thr Gly	
	660 665 670	
	GGC TTT TAC GGC CCG CAG GCG GAG GAA TTG GGC GGT ACT ATT TTC AAT	2064
	Gly Phe Tyr Gly Pro Gln Ala Glu Glu Leu Gly Gly Thr Ile Phe Asn	
20	675 680 685	
	AAT GAT GGG AAA TCT CTT GGT ATA ACT GAA GAT ACT GAA AAT GAA GCT	2112
	Asn Asp Gly Lys Ser Leu Gly Ile Thr Glu Asp Thr Glu Asn Glu Ala	
	690 695 700	
25	GAA GCT GAA GTT GAA AAT GAA GCT GGT GTT GGC GAA CAG TTA AAA CCT	2160
	Glu Ala Glu Val Glu Asn Glu Ala Gly Val Gly Glu Gln Leu Lys Pro	
	705 710 715 720	
30	GAA GCT AAA CCC CAA TTC GGC GTG GTA TTC GGT GCG AAG AAA GAT AAT	2208
	Glu Ala Lys Pro Gln Phe Gly Val Val Phe Gly Ala Lys Lys Asp Asn	
	725 730 735	
	AAA GAG GTG GAA AAA TGA	2226
35	Lys Glu Val Glu Lys	
	740	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(B) STRAIN: *Neisseria meningitidis* strain H44/76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
 1 5 10 15
 Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
 20 25 30
 Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
 35 40 45
 Pro Pro Pro Ala Lys Pro Ser Ile Glu Thr Thr Pro Val Pro Ser Thr
 50 55 60
 Gly Pro Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Ile Phe Ala
 65 70 75 80
 Thr Ser Asp Lys Val Gly Asn Asp Phe Pro Asn Ser Lys Gln Ala Glu
 85 90 95
 Glu Lys Leu Ser Phe Lys Glu Gly Asp Val Leu Phe Leu Tyr Gly Ser
 100 105 110
 Lys Lys Asp Lys Leu Gln Trp Leu Lys Asp Lys Ile His Gln Arg Asn
 115 120 125
 Pro Asn Val Glu Ile Arg Thr Ser Glu Asn Glu Asn Lys Lys Tyr Gly
 130 135 140
 Tyr Glu Phe Val Asp Ala Gly Tyr Val Tyr Thr Lys Asn Gly Thr Asp
 145 150 155 160
 Glu Ile Glu Trp Thr Ser Asn Arg Lys Gln Phe Ser Asn Arg Phe Gly
 165 170 175
 Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu His Pro Ser Gln Ser Leu
 180 185 190
 Pro Ser Ala Gly Thr Val Gln Tyr Ser Gly Asn Trp Gln Tyr Met Thr
 195 200 205
 Asp Ala Ile Arg His Arg Thr Gly Lys Ala Gly Asp Pro Ser Glu Asp
 210 215 220

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Leu Gly Tyr Leu Val Tyr Tyr Gly Gln Asn Val Gly Ala Thr Ser Tyr
 225 230 235 240
 Ala Ala Thr Ala Asp Asp Arg Glu Gly Lys His Pro Ala Glu Tyr Thr
 245 250 255
 5 Val Asp Phe Asp Lys Lys Thr Leu Thr Gly Gln Leu Ile Lys Asn Gln
 260 265 270
 Tyr Val Gln Lys Lys Thr Asp Glu Lys Lys Pro Leu Thr Ile Tyr Asp
 275 280 285
 Ile Thr Ala Thr Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val
 10 290 295 300
 Asn Thr Glu Leu Lys Thr Ser His Ala Asp Lys Glu His Leu Phe Phe
 305 310 315 320
 His Thr Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys
 325 330 335
 15 Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe
 340 345 350
 Gly Val Phe Ala Gly Lys Lys Thr Asn Ala Ser Asn Ala Ala Asp Thr
 355 360 365
 Asn Pro Ala Met Pro Ser Glu Lys His Thr Lys Ile Leu Asp Ser Leu
 20 370 375 380
 Lys Ile Ser Val Asp Glu Ala Thr Asp Lys Asn Ala Arg Pro Phe Ala
 385 390 395 400
 Ile Ser Pro Leu Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu
 405 410 415
 25 Gly Arg Glu Ile Pro Leu Val Ser Gln Glu Lys Thr Ile Glu Leu Ala
 420 425 430
 Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr
 435 440 445
 Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys Pro Lys
 30 450 455 460
 Ala Glu Asp Lys Gly Lys Asp Glu Glu Asp Thr Gly Val Gly Asn Asp
 465 470 475 480
 Glu Glu Gly Thr Glu Asp Glu Ala Ala Glu Gly Ser Glu Gly Gly Glu
 485 490 495
 35 Asp Glu Ile Gly Asp Glu Gly Gly Gly Ala Glu Asp Glu Ala Ala Glu
 500 505 510
 Asn Glu Gly Gly Glu Glu Asp Glu Ala Glu Glu Pro Glu Glu Pro Glu
 515 520 525
 Glu Glu Ser Pro Ala Glu Gly Gly Gly Gly Gly Ser Asp Gly Ile Leu
 40 530 535 540
 Pro Ala Pro Glu Ala Pro Lys Gly Arg Asp Ile Asp Leu Phe Leu Lys
 545 550 555 560

(2) INFORMATION FOR SEQ ID NO:7:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA
(vi) ORIGINAL SOURCE:
(B) STRAIN: Neisseria meningitidis strain M990
(ix) FEATURE:

40 (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...2259
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5	ATG TGT AAA CCG AAT TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTA	48
	Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu	
	1 5 10 15	
10	GCA TCT TGT ATC GGC GGC AAT TTC GGC GTA CAG CCT GTT GTC GAA TCA	96
	Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser	
	20 25 30	
15	ACG CCG ACC GCG CCA ACT CTG TCA GAT TCC AAA TCT TCC AAT CCT GCG	144
	Thr Pro Thr Ala Pro Thr Leu Ser Asp Ser Lys Ser Ser Asn Pro Ala	
	35 40 45	
20	GAT AAG CCT GCT CCA GCT CCT GCC GAG CCT TCG GTA GAA ATC ACG CCG	192
	Asp Lys Pro Ala Pro Ala Pro Ala Glu Pro Ser Val Glu Ile Thr Pro	
	50 55 60	
25	GTC AAG CGG CCC GCC GTC GGT GCG GCA ATG CGG CTG CCA AGG CGG AAT	240
	Val Lys Arg Pro Ala Val Gly Ala Ala Met Arg Leu Pro Arg Arg Asn	
	65 70 75 80	
30	ATC GCA ACT TTT GAT AAA AAT GGT AAT GAA ATT CCC AAT AGT AAG CAG	288
	Ile Ala Thr Phe Asp Lys Asn Gly Asn Glu Ile Pro Asn Ser Lys Gln	
	85 90 95	
35	GCA GAG GAG TAT CTG CCG CTC AAA GAG AAG GAT ATC CTG TTT TTA GAC	336
	Ala Glu Glu Tyr Leu Pro Leu Lys Glu Lys Asp Ile Leu Phe Leu Asp	
	100 105 110	
40	GGT ACG CCG AAA GAA CAG GCT GAC AAA CTT AAA AAG GAA ATC AAC GGA	384
	Gly Thr Pro Lys Glu Gln Ala Asp Lys Leu Lys Lys Glu Ile Asn Gly	
	115 120 125	
45	CGG CAT CCT AAT GCA CCA ATC TAC ACG TCC GAT TTA AAA GAT GAT GCG	432
	Arg His Pro Asn Ala Pro Ile Tyr Thr Ser Asp Leu Lys Asp Asp Ala	
	130 135 140	
50	TAT CAA TAT AAA TAT GTC CGG GCC GGA TAT GTT TAT ACT AGA TAT GGA	480
	Tyr Gln Tyr Lys Tyr Val Arg Ala Gly Tyr Val Tyr Thr Arg Tyr Gly	
	145 150 155 160	

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	ACA GAT GAA ATC GAA CAG AAC TCA GGC GGT AAG CGG GTT ACC CAC CGC	528
	Thr Asp Glu Ile Glu Gln Asn Ser Gly Gly Lys Arg Val Thr His Arg	
	165 170 175	
5	TTA GGT TAT GAC GGT TTT GTA TAT TAT TCC GGA GAA CGT CCT TCC CAA	576
	Leu Gly Tyr Asp Gly Phe Val Tyr Tyr Ser Gly Glu Arg Pro Ser Gln	
	180 185 190	
10	TCT TTA CCG AGT GCG GGA ACG GTG GAA TAT TCT GGT AAC TGG CAA TAT	624
	Ser Leu Pro Ser Ala Gly Thr Val Glu Tyr Ser Gly Asn Trp Gln Tyr	
	195 200 205	
15	ATG ACC GAT GCC AAA CGT CAT CGA GCA GGT CAG GCG GTT GGC ATT GAC	672
	Met Thr Asp Ala Lys Arg His Arg Ala Gly Gln Ala Val Gly Ile Asp	
	210 215 220	
20	AAT TTG GGT TAT ATC ACA TTT TAT GGT AAC GAT GTT GGT GCA ACT TCT	720
	Asn Leu Gly Tyr Ile Thr Phe Tyr Gly Asn Asp Val Gly Ala Thr Ser	
	225 230 235 240	
	TAT GCG GCT AAG GAT GTC GAC GAA AGG GAA AAG CAT CCT GCC AAA TAT	768
	Tyr Ala Ala Lys Asp Val Asp Glu Arg Glu Lys His Pro Ala Lys Tyr	
	245 250 255	
25	ACG GTT GAT TTT GAT AAC AAA ACC ATG AAT GGC AAG CTG ATT AAA AAT	816
	Thr Val Asp Phe Asp Asn Lys Thr Met Asn Gly Lys Leu Ile Lys Asn	
	260 265 270	
30	CAG TAT GTG CGA AAT AAA AAA GAT GAA CCC AAA AAA CCG CTG ACC ATT	864
	Gln Tyr Val Arg Asn Lys Lys Asp Glu Pro Lys Lys Pro Leu Thr Ile	
	275 280 285	
35	TAC GAC ATT ACT GCA AAA TTG GAC GGC AAC CGC TTT ACC GGC AGT GCC	912
	Tyr Asp Ile Thr Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala	
	290 295 300	
40	AAG GTC AAT CCT GAT TTA GCG AAA AAC CTT GCC GGT AAT GAG CGT TTG	960
	Lys Val Asn Pro Asp Leu Ala Lys Asn Leu Ala Gly Asn Glu Arg Leu	
	305 310 315 320	
	TTT TTC CAT GCC GAT GCC GAT CAG CGG CTT GAG GGC GGT TTT TTC GGC	1008
	Phe Phe His Ala Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly	
	325 330 335	

	GAT AAC GGA GAA GAG CTT GCC GGA CGG TTT ATC AGC AAC GAC AAC AGC	1056
	Asp Asn Gly Glu Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser	
	340 345 350	
5	GTA TTC GGC GTA TTC GCA GGC AAA AAA ACA GAG ACA GCA AAC GCA GCA	1104
	Val Phe Gly Val Phe Ala Gly Lys Lys Thr Glu Thr Ala Asn Ala Ala	
	355 360 365	
10	GAT ACA AAA CCT GCC CTG CCG TCT GGA AAA CAC ACC AAA ATC TTG GAT	1152
	Asp Thr Lys Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp	
	370 375 380	
15	TCT CTA AAA ATT TCC GTT GAC GAG GCG ACT GAT GGC CAT GCC CGT AAG	1200
	Ser Leu Lys Ile Ser Val Asp Glu Ala Thr Asp Gly His Ala Arg Lys	
	385 390 395 400	
20	TTT GCC ATT TCC TCT ATG CCC GAT TTT GGT CAT CCC GAC AAA CTT CTT	1248
	Phe Ala Ile Ser Ser Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu	
	405 410 415	
25	GTC GAA GGG CGT GAA ATT CCT TTG GTA AAC GAA GAA CAA ATC ATC AAG	1296
	Val Glu Gly Arg Glu Ile Pro Leu Val Asn Glu Glu Gln Ile Ile Lys	
	420 425 430	
30	CTT GCC GAC GGC AGG AAA ATG ACC GTC CGT GCT TGT TGC GAC TTT TTG	1344
	Leu Ala Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu	
	435 440 445	
35	ACC TAT GTG AAA CTC GGA CGG ATA AAA ACC GAT CGC CCG GCA AGT AAA	1392
	Thr Tyr Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys	
	450 455 460	
40	CCA AAG GCG GAA GAT AAA GGG GAG GAT GAA GAG GGT GCA GGC GTT GAT	1440
	Pro Lys Ala Glu Asp Lys Gly Glu Asp Glu Glu Gly Ala Gly Val Asp	
	465 470 475 480	
	AAC GAC GAA GAA AGC GAA GAC GAA GCC GTA GAA GAC GAA GGC GGC GAA	1488
	Asn Asp Glu Glu Ser Glu Asp Glu Ala Val Glu Asp Glu Gly Gly Glu	
	485 490 495	

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	GAA GAC GAA ACT TCC GAA GAG GAT AAT GGC GAA GAC GAA GAA GCA ACC	1536
	Glu Asp Glu Thr Ser Glu Glu Asp Asn Gly Glu Asp Glu Glu Ala Thr	
	500 505 510	
5	GCC GAA GAA GAA ACC GAA GAA GTT GAT GAA GCC GAA GAG GAG GAA GTT	1584
	Ala Glu Glu Glu Thr Glu Glu Val Asp Glu Ala Glu Glu Glu Glu Val	
	515 520 525	
10	GAA GAA CCC GAA GAA AAA TCG CCG GCA GAA GGC AAC GGC GGT TCA GGC	1632
	Glu Glu Pro Glu Glu Lys Ser Pro Ala Glu Gly Asn Gly Gly Ser Gly	
	530 535 540	
	AGC ATC CTG CCT GCC CTA GAA GCC TCT AAA GGC AGG GAC ATC GAC CTT	1680
	Ser Ile Leu Pro Ala Leu Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu	
15	545 550 555 560	
	TTC CTG AAA GGT ATC CGC ACG GCA GAA ACG GAT ATT CCG CAA AGC GGA	1728
	Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr Asp Ile Pro Gln Ser Gly	
	565 570 575	
20	ACG GCG CAT TAT ACC GGC ACT TGG GAA GCG CGT ATC GGC AAA CCC ATT	1776
	Thr Ala His Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Lys Pro Ile	
	580 585 590	
25	CAA TGG GAC AAT CAG GCG GAT GAA AAA GCG GCA AAA GCA GAA TTT ACC	1824
	Gln Trp Asp Asn Gln Ala Asp Glu Lys Ala Ala Lys Ala Glu Phe Thr	
	595 600 605	
	GTT GAT TTC GAC AAG AAA TCG ATT TCC GGA AAG CTG ACG GAG CAA AAC	1872
30	Val Asp Phe Asp Lys Lys Ser Ile Ser Gly Lys Leu Thr Glu Gln Asn	
	610 615 620	
	GGC GTA GAA CCT GCT TTC CAT ATT GAA GAC GGC AAG ATT GAT GGC AAC	1920
	Gly Val Glu Pro Ala Phe His Ile Glu Asp Gly Lys Ile Asp Gly Asn	
35	625 630 635 640	
	GGT TTC CAC GCG ACA GCG CGC ACT CGG GAG AGC GGC ATC AAT CTT TCG	1968
	Gly Phe His Ala Thr Ala Arg Thr Arg Glu Ser Gly Ile Asn Leu Ser	
	645 650 655	
40	GGA AAT GGT TCG ACC GAC CCC AAA ACA TTC CAA GCT AGT AAT CTT CGT	2016
	Gly Asn Gly Ser Thr Asp Pro Lys Thr Phe Gln Ala Ser Asn Leu Arg	
	660 665 670	

5 GTA GAA GGA GGA TTT TAC GGC CCG CAG GCG GCG GAA TTG GGC GGT ACT 2064
 Val Glu Gly Gly Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Thr
 675 680 685

10 ATT TTC AAT AAT GAT GGG AAA TCT CTT AGT ATA ACT GAA AAT ATT GAA 2112
 Ile Phe Asn Asn Asp Gly Lys Ser Leu Ser Ile Thr Glu Asn Ile Glu
 690 695 700

15 AAT GAA GCT GAA GCT GAA GTT GAA GTT GAA GCT GAA GCT GAA GTT GAA 2160
 Asn Glu Ala Glu Ala Glu Val Glu Val Glu Ala Glu Ala Glu Val Glu
 705 710 715 720

20 GTT GAA GCT GAT GTT GGC AAA CAG TTA GAA CCT GAT GAA GTT AAA CAC 2208
 Val Glu Ala Asp Val Gly Lys Gln Leu Glu Pro Asp Glu Val Lys His
 725 730 735

25 AAA TTC GGC GTG GTA TTC GGT GCG AAG AAA GAT ATG CAG GAG GTG GAA 2256
 Lys Phe Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val Glu
 740 745 750

30 AAA TGA 2262
 Lys

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 753 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(B) STRAIN: *Neisseria meningitidis* strain M990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
 1 5 10 15

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	Ala	Ser	Cys	Ile	Gly	Gly	Asn	Phe	Gly	Val	Gln	Pro	Val	Val	Glu	Ser
				20					25						30	
	Thr	Pro	Thr	Ala	Pro	Thr	Leu	Ser	Asp	Ser	Lys	Ser	Ser	Asn	Pro	Ala
			35					40					45			
5	Asp	Lys	Pro	Ala	Pro	Ala	Pro	Ala	Glu	Pro	Ser	Val	Glu	Ile	Thr	Pro
		50					55					60				
	Val	Lys	Arg	Pro	Ala	Val	Gly	Ala	Ala	Met	Arg	Leu	Pro	Arg	Arg	Asn
	65					70				75					80	
	Ile	Ala	Thr	Phe	Asp	Lys	Asn	Gly	Asn	Glu	Ile	Pro	Asn	Ser	Lys	Gln
10				85						90					95	
	Ala	Glu	Glu	Tyr	Leu	Pro	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Phe	Leu	Asp
				100					105					110		
	Gly	Thr	Pro	Lys	Glu	Gln	Ala	Asp	Lys	Leu	Lys	Lys	Glu	Ile	Asn	Gly
				115				120					125			
15	Arg	His	Pro	Asn	Ala	Pro	Ile	Tyr	Thr	Ser	Asp	Leu	Lys	Asp	Asp	Ala
		130					135					140				
	Tyr	Gln	Tyr	Lys	Tyr	Val	Arg	Ala	Gly	Tyr	Val	Tyr	Thr	Arg	Tyr	Gly
	145				150					155					160	
	Thr	Asp	Glu	Ile	Glu	Gln	Asn	Ser	Gly	Gly	Lys	Arg	Val	Thr	His	Arg
20				165						170					175	
	Leu	Gly	Tyr	Asp	Gly	Phe	Val	Tyr	Tyr	Ser	Gly	Glu	Arg	Pro	Ser	Gln
				180					185				190			
	Ser	Leu	Pro	Ser	Ala	Gly	Thr	Val	Glu	Tyr	Ser	Gly	Asn	Trp	Gln	Tyr
		195					200					205				
25	Met	Thr	Asp	Ala	Lys	Arg	His	Arg	Ala	Gly	Gln	Ala	Val	Gly	Ile	Asp
		210					215					220				
	Asn	Leu	Gly	Tyr	Ile	Thr	Phe	Tyr	Gly	Asn	Asp	Val	Gly	Ala	Thr	Ser
	225					230				235					240	
	Tyr	Ala	Ala	Lys	Asp	Val	Asp	Glu	Arg	Glu	Lys	His	Pro	Ala	Lys	Tyr
30				245						250					255	
	Thr	Val	Asp	Phe	Asp	Asn	Lys	Thr	Met	Asn	Gly	Lys	Leu	Ile	Lys	Asn
				260					265					270		
	Gln	Tyr	Val	Arg	Asn	Lys	Lys	Asp	Glu	Pro	Lys	Lys	Pro	Leu	Thr	Ile
				275				280					285			
35	Tyr	Asp	Ile	Thr	Ala	Lys	Leu	Asp	Gly	Asn	Arg	Phe	Thr	Gly	Ser	Ala
		290					295					300				
	Lys	Val	Asn	Pro	Asp	Leu	Ala	Lys	Asn	Leu	Ala	Gly	Asn	Glu	Arg	Leu
	305					310				315					320	
	Phe	Phe	His	Ala	Asp	Ala	Asp	Gln	Arg	Leu	Glu	Gly	Gly	Phe	Phe	Gly
40				325						330					335	
	Asp	Asn	Gly	Glu	Glu	Leu	Ala	Gly	Arg	Phe	Ile	Ser	Asn	Asp	Asn	Ser
				340					345					350		

32

Val Phe Gly Val Phe Ala Gly Lys Lys Thr Glu Thr Ala Asn Ala Ala
 355 360 365
 Asp Thr Lys Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp
 370 375 380
 5 Ser Leu Lys Ile Ser Val Asp Glu Ala Thr Asp Gly His Ala Arg Lys
 385 390 395 400
 Phe Ala Ile Ser Ser Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu
 405 410 415
 10 Val Glu Gly Arg Glu Ile Pro Leu Val Asn Glu Glu Gln Ile Ile Lys
 420 425 430
 Leu Ala Asp Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu
 435 440 445
 Thr Tyr Val Lys Leu Gly Arg Ile Lys Thr Asp Arg Pro Ala Ser Lys
 450 455 460
 15 Pro Lys Ala Glu Asp Lys Gly Glu Asp Glu Glu Gly Ala Gly Val Asp
 465 470 475 480
 Asn Asp Glu Glu Ser Glu Asp Glu Ala Val Glu Asp Glu Gly Gly Glu
 485 490 495
 Glu Asp Glu Thr Ser Glu Glu Asp Asn Gly Glu Asp Glu Glu Ala Thr
 20 500 505 510
 Ala Glu Glu Glu Thr Glu Glu Val Asp Glu Ala Glu Glu Glu Val
 515 520 525
 Glu Glu Pro Glu Glu Lys Ser Pro Ala Glu Gly Asn Gly Gly Ser Gly
 530 535 540
 25 Ser Ile Leu Pro Ala Leu Glu Ala Ser Lys Gly Arg Asp Ile Asp Leu
 545 550 555 560
 Phe Leu Lys Gly Ile Arg Thr Ala Glu Thr Asp Ile Pro Gln Ser Gly
 565 570 575
 Thr Ala His Tyr Thr Gly Thr Trp Glu Ala Arg Ile Gly Lys Pro Ile
 30 580 585 590
 Gln Trp Asp Asn Gln Ala Asp Glu Lys Ala Ala Lys Ala Glu Phe Thr
 595 600 605
 Val Asp Phe Asp Lys Lys Ser Ile Ser Gly Lys Leu Thr Glu Gln Asn
 610 615 620
 35 Gly Val Glu Pro Ala Phe His Ile Glu Asp Gly Lys Ile Asp Gly Asn
 625 630 635 640
 Gly Phe His Ala Thr Ala Arg Thr Arg Glu Ser Gly Ile Asn Leu Ser
 645 650 655
 Gly Asn Gly Ser Thr Asp Pro Lys Thr Phe Gln Ala Ser Asn Leu Arg
 40 660 665 670
 Val Glu Gly Gly Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Thr
 675 680 685

33

Ile Phe Asn Asn Asp Gly Lys Ser Leu Ser Ile Thr Glu Asn Ile Glu
 690 695 700
 Asn Glu Ala Glu Ala Glu Val Glu Val Glu Ala Glu Ala Glu Val Glu
 705 710 715 720
 5 Val Glu Ala Asp Val Gly Lys Gln Leu Glu Pro Asp Glu Val Lys His
 725 730 735
 Lys Phe Gly Val Val Phe Gly Ala Lys Lys Asp Met Gln Glu Val Glu
 740 745 750
 Lys

10

(2) INFORMATION FOR SEQ ID NO:9:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2124 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

20

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(B) STRAIN: Neisseria meningitidis strain 881607

25

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...2121

(D) OTHER INFORMATION:

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TGT AAA CCG AAT TAT GGC GGC ATT GTC TTG TTG CCC TTA CTT TTG 48
 Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
 35 1 5 10 15
 GCA TCT TGC ATC GGC GGC AAT TTC GGC GTG CAG CCT GTT GTC GAA TCA 96
 Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
 20 25 30
 40 ACG CCG ACC GCG TAC CCC GTC ACT TTC AAG TCT AAG GAC GTT CCC ACT 144
 Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
 35 40 45

	TCG CCT CCT GCC GGG TCT TCG GTA GAA ACC ACG CCG GTC AAC CGA CCC	192
	Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Arg Pro	
	50 55 60	
5	GCC GTT GGT GCG GCA ATG CGG CTG TTG AGA CGG AAT ATT GCA ACT TCT	240
	Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Ile Ala Thr Ser	
	65 70 75 80	
10	GAT AAG GAT GGC AAT GAT TTT CCA AAT AGC AAA CAA GCA GAA GAA AAG	288
	Asp Lys Asp Gly Asn Asp Phe Pro Asn Ser Lys Gln Ala Glu Glu Lys	
	85 90 95	
15	CTG TCG TTT AAA GAG GAA GAT ATC CTG TTT TTA TAC GGT TCC AAA AAA	336
	Leu Ser Phe Lys Glu Glu Asp Ile Leu Phe Leu Tyr Gly Ser Lys Lys	
	100 105 110	
20	GAT CAA CGT CAG CAG CTT AAA GAT AAA ATT CGT CAA CCA AAT CCT ACG	384
	Asp Gln Arg Gln Gln Leu Lys Asp Lys Ile Arg Gln Pro Asn Pro Thr	
	115 120 125	
25	GCA AGC ATT ACC ACA TCG GAA AAG AAA AAT AAA AAA TAT GAT TAT AAA	432
	Ala Ser Ile Thr Thr Ser Glu Lys Lys Asn Lys Lys Tyr Asp Tyr Lys	
	130 135 140	
30	TTT GTA GAT GCA GGT TAT GTA TAT ACT AAA GAC GGA AAA GAT GAA ATT	480
	Phe Val Asp Ala Gly Tyr Val Tyr Thr Lys Asp Gly Lys Asp Glu Ile	
	145 150 155 160	
35	GAG TGG ACT TCA AAT TAC AAG CAG TCT ACC AAC CCG TTT GGT TAT GAC	528
	Glu Trp Thr Ser Asn Tyr Lys Gln Ser Thr Asn Arg Phe Gly Tyr Asp	
	165 170 175	
40	GGT TTT GTA TAT TAT TCC GGA GAA CAT CCT TCG CAA TCT TTA CCG AGC	576
	Gly Phe Val Tyr Tyr Ser Gly Glu His Pro Ser Gln Ser Leu Pro Ser	
	180 185 190	
45	GCG GGA ACG GTG AAA TAT TCC GGC AAC TGG CAA TAT ATG ACC GAT GCC	624
	Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala	
	195 200 205	

35

	ATA CGT CAT CGA ACA GGA AAA GCA GGA GAT CCT AGC GAA GAT TTG GGT	672
	Ile Arg His Arg Thr Gly Lys Ala Gly Asp Pro Ser Glu Asp Leu Gly	
	210 215 220	
5	TAT ATC GTT TAT TAC GGT CAA AAT GTC GGA GCA ACT TCT TAT GCT GCG	720
	Tyr Ile Val Tyr Tyr Gly Gln Asn Val Gly Ala Thr Ser Tyr Ala Ala	
	225 230 235 240	
10	ACT GCC GAC GAC CGG GAG GGA AAA CAT CCT GCC GAA TAT ACG GTT AAT	768
	Thr Ala Asp Asp Arg Glu Gly Lys His Pro Ala Glu Tyr Thr Val Asn	
	245 250 255	
15	TTC GAC CAA AAA ACT CTG AAT GGC AAG CTG ATT AAA AAT CAG TAT GTG	816
	Phe Asp Gln Lys Thr Leu Asn Gly Lys Leu Ile Lys Asn Gln Tyr Val	
	260 265 270	
20	CAA AAG AGA GAT GAT CCT AAA AAA CCA CTG ACC ATT TAC GAC ATT ACT	864
	Gln Lys Arg Asp Asp Pro Lys Lys Pro Leu Thr Ile Tyr Asp Ile Thr	
	275 280 285	
25	GCA AAA TTG GAC GGC AAC CGC TTT ACC GGC AGT GCC AAA GTT AAC ACA	912
	Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn Thr	
	290 295 300	
30	GAG GTG AAG ACG AAT CAC GCT GAT AAA GAA TAT TTG TTT TTC CAT ACC	960
	Glu Val Lys Thr Asn His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr	
	305 310 315 320	
35	GAT GCC GAT CAG CGG CTT GAG GGC GGT TTT TTC GGC GAT AAG GGG GAA	1008
	Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys Gly Glu	
	325 330 335	
40	GAG CTT GCC GGA CGG TTT ATC AGC AAC GAC AAC AGC GTA TTC GGC GTG	1056
	Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val	
	340 345 350	
45	TTC GCA GGC AAA CAA AAA ACA GAG ACA GCA AAC GCA TCA GAT ACA AAT	1104
	Phe Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn	
	355 360 365	
50	CCT GCC CTG CCG TCT GGA AAA CAC ACC AAA ATC TTG GAT TCT CTA AAA	1152
	Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys	
	370 375 380	

5	ATT TCC GTT GAC GAG GCA AGT GGT GAA AAT CCC CGA CCG TTT GAG GTT	1200
	Ile Ser Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro Phe Glu Val	
	385 390 395 400	
	TCC ACT ATG CCC GAT TTT GGT CAT CCC GAC AAA CTT CTT GTC GAA GGG	1248
	Ser Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly	
10	CGT GAA ATT CCT TTG GTA AAC AAA GAA CAA ACC ATC GAT CTT GCC GAC	1296
	Arg Glu Ile Pro Leu Val Asn Lys Glu Gln Thr Ile Asp Leu Ala Asp	
	420 425 430	
	GGC AGG AAA ATG ACC GTC CGT GCT TGT TGC GAC TTT TTG ACC TAT GTG	1344
	Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val	
15	AAA CTC GGA CGG ATA AAA ACC GAA CGC CCC GCC GTC CAA CCG AAG GCG	1392
	Lys Leu Gly Arg Ile Lys Thr Glu Arg Pro Ala Val Gln Pro Lys Ala	
	450 455 460	
	CAG GAT GAA GAG GGG GAC GAA GAG GGT GTA GGC GTT GAT AAC GGT AAA	1440
	Gln Asp Glu Glu Gly Asp Glu Glu Gly Val Gly Val Asp Asn Gly Lys	
20	GAA AGC GAA GAC GAA ATC GGC GAT GAA GAA AGC ACC GGA GAC GAA GTC	1488
	Glu Ser Glu Asp Glu Ile Gly Asp Glu Glu Ser Thr Gly Asp Glu Val	
	485 490 495	
	GTA GAA GAT GAA GAC GAA GAT GAA GAC GAA GAA GAA ATC GAA GAA GAA	1536
	Val Glu Asp Glu Asp Glu Asp Glu Asp Glu Glu Glu Ile Glu Glu Glu	
25	CCT GAA GAA GAA GCT GAA GAG GAA GAA CCC GAA GAA GAA TTG CCG GCA	1584
	Pro Glu Glu Glu Ala Glu Glu Glu Glu Pro Glu Glu Glu Leu Pro Ala	
	515 520 525	
	GAA GAA GGC AAC GGC GGT TCA GGC AGC ATC CTG CCC ACT CCG GAA GCC	1632
	Glu Glu Gly Asn Gly Gly Ser Gly Ser Ile Leu Pro Thr Pro Glu Ala	
30	GAA GAA GGC AAC GGC GGT TCA GGC AGC ATC CTG CCC ACT CCG GAA GCC	1632
	Glu Glu Gly Asn Gly Gly Ser Gly Ser Ile Leu Pro Thr Pro Glu Ala	
	530 535 540	

PCT/EP98/05117

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(2) INFORMATION FOR SEQ ID NO:10:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(B) STRAIN: *Neisseria meningitidis* strain 881607

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Met Cys Lys Pro Asn Tyr Gly Gly Ile Val Leu Leu Pro Leu Leu Leu
 1             5             10             15
20 Ala Ser Cys Ile Gly Gly Asn Phe Gly Val Gln Pro Val Val Glu Ser
    20             25             30
Thr Pro Thr Ala Tyr Pro Val Thr Phe Lys Ser Lys Asp Val Pro Thr
    35             40             45
Ser Pro Pro Ala Gly Ser Ser Val Glu Thr Thr Pro Val Asn Arg Pro
25    50             55             60
Ala Val Gly Ala Ala Met Arg Leu Leu Arg Arg Asn Ile Ala Thr Ser
65             70             75             80
Asp Lys Asp Gly Asn Asp Phe Pro Asn Ser Lys Gln Ala Glu Glu Lys
    85             90             95
30 Leu Ser Phe Lys Glu Glu Asp Ile Leu Phe Leu Tyr Gly Ser Lys Lys
    100             105             110
Asp Gln Arg Gln Gln Leu Lys Asp Lys Ile Arg Gln Pro Asn Pro Thr
    115             120             125
Ala Ser Ile Thr Thr Ser Glu Lys Lys Asn Lys Lys Tyr Asp Tyr Lys
35    130             135             140
Phe Val Asp Ala Gly Tyr Val Tyr Thr Lys Asp Gly Lys Asp Glu Ile
145             150             155             160
Glu Trp Thr Ser Asn Tyr Lys Gln Ser Thr Asn Arg Phe Gly Tyr Asp
    165             170             175
40 Gly Phe Val Tyr Tyr Ser Gly Glu His Pro Ser Gln Ser Leu Pro Ser
    180             185             190
Ala Gly Thr Val Lys Tyr Ser Gly Asn Trp Gln Tyr Met Thr Asp Ala
    195             200             205

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Ile Arg His Arg Thr Gly Lys Ala Gly Asp Pro Ser Glu Asp Leu Gly
 210 215 220
 Tyr Ile Val Tyr Tyr Gly Gln Asn Val Gly Ala Thr Ser Tyr Ala Ala
 225 230 235 240
 5 Thr Ala Asp Asp Arg Glu Gly Lys His Pro Ala Glu Tyr Thr Val Asn
 245 250 255
 Phe Asp Gln Lys Thr Leu Asn Gly Lys Leu Ile Lys Asn Gln Tyr Val
 260 265 270
 10 Gln Lys Arg Asp Asp Pro Lys Lys Pro Leu Thr Ile Tyr Asp Ile Thr
 275 280 285
 Ala Lys Leu Asp Gly Asn Arg Phe Thr Gly Ser Ala Lys Val Asn Thr
 290 295 300
 Glu Val Lys Thr Asn His Ala Asp Lys Glu Tyr Leu Phe Phe His Thr
 305 310 315 320
 15 Asp Ala Asp Gln Arg Leu Glu Gly Gly Phe Phe Gly Asp Lys Gly Glu
 325 330 335
 Glu Leu Ala Gly Arg Phe Ile Ser Asn Asp Asn Ser Val Phe Gly Val
 340 345 350
 Phe Ala Gly Lys Gln Lys Thr Glu Thr Ala Asn Ala Ser Asp Thr Asn
 355 360 365
 20 Pro Ala Leu Pro Ser Gly Lys His Thr Lys Ile Leu Asp Ser Leu Lys
 370 375 380
 Ile Ser Val Asp Glu Ala Ser Gly Glu Asn Pro Arg Pro Phe Glu Val
 385 390 395 400
 25 Ser Thr Met Pro Asp Phe Gly His Pro Asp Lys Leu Leu Val Glu Gly
 405 410 415
 Arg Glu Ile Pro Leu Val Asn Lys Glu Gln Thr Ile Asp Leu Ala Asp
 420 425 430
 Gly Arg Lys Met Thr Val Arg Ala Cys Cys Asp Phe Leu Thr Tyr Val
 435 440 445
 30 Lys Leu Gly Arg Ile Lys Thr Glu Arg Pro Ala Val Gln Pro Lys Ala
 450 455 460
 Gln Asp Glu Glu Gly Asp Glu Glu Gly Val Gly Val Asp Asn Gly Lys
 465 470 475 480
 35 Glu Ser Glu Asp Glu Ile Gly Asp Glu Glu Ser Thr Gly Asp Glu Val
 485 490 495
 Val Glu Asp Glu Asp Glu Asp Glu Asp Glu Glu Glu Ile Glu Glu Glu
 500 505 510
 Pro Glu Glu Glu Ala Glu Glu Glu Glu Pro Glu Glu Glu Leu Pro Ala
 515 520 525
 40 Glu Glu Gly Asn Gly Gly Ser Gly Ser Ile Leu Pro Thr Pro Glu Ala
 530 535 540

Ser Lys Gly Arg Asp Ile Asp Leu Phe Leu Lys Gly Ile Arg Thr Ala
 545 550 555 560
 Glu Ala Asp Ile Pro Lys Asn Gly Thr Ala His Tyr Thr Gly Thr Trp
 565 570 575
 5 Glu Ala Arg Ile Gly Val Ser Asp Ser Gly Thr Ser Ile Gln Lys Asp
 580 585 590
 Ser Tyr Ala Asn Gln Gly Ala Lys Ala Glu Phe Thr Val Asp Phe Glu
 595 600 605
 Ala Lys Thr Val Ser Gly Met Leu Thr Glu Lys Asn Asp Thr Thr Pro
 10 610 615 620
 Ala Phe Tyr Ile Glu Lys Gly Val Ile Asp Gly Asn Gly Phe His Ala
 625 630 635 640
 Leu Ala His Thr Arg Glu Asn Gly Ile Asp Leu Ser Gly Gln Gly Ser
 645 650 655
 15 Thr Asn Pro Lys Asn Phe Lys Ala Asp Asn Leu Leu Val Thr Gly Gly
 660 665 670
 Phe Tyr Gly Pro Gln Ala Ala Glu Leu Gly Gly Asn Ile Ile Asp Ser
 675 680 685
 Asp Arg Lys Phe Gly Ala Val Phe Gly Ala Lys Lys Asp Asp Lys Glu
 20 690 695 700
 Ala Thr Arg
 705